

#5



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PCT10

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/10/088,830

DATE: 04/09/2002
 TIME: 13:06:06

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3 <110> APPLICANT: Gutierrez-Armenta, Crisanto
4   Ramirez-Parra, Elena
6 <120> TITLE OF INVENTION: Wheat DP Proteins And Uses Thereof
8 <130> FILE REFERENCE: BTGI-0025
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/088,830
C--> 10 <141> CURRENT FILING DATE: 2002-03-22
10 <150> PRIOR APPLICATION NUMBER: P9902127
11 <151> PRIOR FILING DATE: 1999-09-24
13 <150> PRIOR APPLICATION NUMBER: PCT/EP00/09325
14 <151> PRIOR FILING DATE: 2000-09-25
16 <150> PRIOR APPLICATION NUMBER: P9902474
17 <151> PRIOR FILING DATE: 1999-11-11
19 <160> NUMBER OF SEQ ID NOS: 16
21 <170> SOFTWARE: PatentIn version 3.1
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24 <211> LENGTH: 1089
25 <212> TYPE: DNA
26 <213> ORGANISM: Triticum monococcum
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39 gct acc gcc gca ctg gac ctg acc ggc gtg cac att ctc gaa gct tcc      100
40 Ala Thr Ala Ala Leu Asp Leu Thr Gly Val His Ile Leu Glu Ala Ser
41                               15           20           25
43 agt gtc ccc ccg ctt ccc gaa gcg ggc ggt aat gcg gtc caa agg aag      148
44 Ser Val Pro Pro Leu Pro Glu Ala Gly Gly Asn Ala Val Gln Arg Lys
45                               30           35           40
47 ggg gct gtt gac ccg gat aaa gat agg aag aag gag aag gct gcg gca      196
48 Gly Ala Val Asp Pro Asp Lys Asp Arg Lys Lys Glu Lys Ala Ala Ala
49                               45           50           55
51 ccg agg atc acc ggt tgg ggg ctc cgc gag tac agc aaa ata gtt tgt      244
52 Pro Arg Ile Thr Gly Trp Gly Leu Arg Glu Tyr Ser Lys Ile Val Cys
53 60                               65           70           75
55 gag aaa gtt gaa gcc aaa gga aga aca aca tac aat gag gtt gca gac      292
56 Glu Lys Val Glu Ala Lys Gly Arg Thr Thr Tyr Asn Glu Val Ala Asp
57                               80           85           90
59 gaa att tat tca gag ctg aag tcc atg gca cat att ggt caa ggg ttt      340
60 Glu Ile Tyr Ser Glu Leu Lys Ser Met Ala His Ile Gly Gln Gly Phe

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61          95          100          105
63 gat gag aag aat att agg cgg aga gtg tat gat gct ttc aac gtt ctc      388
64 Asp Glu Lys Asn Ile Arg Arg Arg Val Tyr Asp Ala Phe Asn Val Leu
65          110          115          120
67 att gca ctt cgt gtt att gca aaa gaa aaa aag gag ata cgg tgg atg      436
68 Ile Ala Leu Arg Val Ile Ala Lys Glu Lys Lys Glu Ile Arg Trp Met
69          125          130          135
71 ggc ctt tca aat tac aga tat gaa aaa ata aag aag ctt gag gaa gtt      484
72 Gly Leu Ser Asn Tyr Arg Tyr Glu Lys Ile Lys Lys Leu Glu Glu Val
73 140          145          150          155
75 cgt aaa gaa ctc gtc aac aag att agg aac aag aag gca ctc ctc cag      532
76 Arg Lys Glu Leu Val Asn Lys Ile Arg Asn Lys Lys Ala Leu Leu Gln
77          160          165          170
79 gaa atc gaa aaa cag ttt gat gat ctc caa aac atc aag tta cgt aac      580
80 Glu Ile Glu Lys Gln Phe Asp Asp Leu Gln Asn Ile Lys Leu Arg Asn
81          175          180          185
83 caa aca ctg gaa agc tca gca gag aat gtt aat ggc atc cgc ctt cca      628
84 Gln Thr Leu Glu Ser Ser Ala Glu Asn Val Asn Gly Ile Arg Leu Pro
85          190          195          200
87 ttc gta ttg gtc aag aca tct agg aaa gca agg gtg gaa att gag att      676
88 Phe Val Leu Val Lys Thr Ser Arg Lys Ala Arg Val Glu Ile Glu Ile
89          205          210          215
91 tca gat gac tcg aag ttt gcc cat ttc gag ttc aat ggt gca cca ttc      724
92 Ser Asp Asp Ser Lys Phe Ala His Phe Glu Phe Asn Gly Ala Pro Phe
93 220          225          230          235
95 aca ttg cat gat gat ctc tca atc ctt gag ggg gta agg cgt aac agc      772
96 Thr Leu His Asp Asp Leu Ser Ile Leu Glu Gly Val Arg Arg Asn Ser
97          240          245          250
99 ata gga aga gct ggc cgc gcc acc ctt cac tagagactca agaattattac      822
100 Ile Gly Arg Ala Gly Arg Ala Thr Leu His
101          255          260
103 aaatgaatta aaagtgttag aactggcaca gccggattct tttgcacagc tatgtatagc      882
105 tatatatcct catgaaaact tgacctagtt tataggacag tctctcaggc ttgagaagat      942
107 tttaacctgc aaattttgtc tcctttttgt gcctagcagg ttattaggtc tcagatagat      1002
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129 Pro Glu Ala Gly Gly Asn Ala Val Gln Arg Lys Gly Ala Val Asp Pro
130          35          40          45
133 Asp Lys Asp Arg Lys Lys Glu Lys Ala Ala Ala Pro Arg Ile Thr Gly
134          50          55          60

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137 Trp Gly Leu Arg Glu Tyr Ser Lys Ile Val Cys Glu Lys Val Glu Ala
138 65              70              75              80
141 Lys Gly Arg Thr Thr Tyr Asn Glu Val Ala Asp Glu Ile Tyr Ser Glu
142              85              90              95
145 Leu Lys Ser Met Ala His Ile Gly Gln Gly Phe Asp Glu Lys Asn Ile
146              100             105             110
149 Arg Arg Arg Val Tyr Asp Ala Phe Asn Val Leu Ile Ala Leu Arg Val
150              115             120             125
153 Ile Ala Lys Glu Lys Lys Glu Ile Arg Trp Met Gly Leu Ser Asn Tyr
154              130             135             140
157 Arg Tyr Glu Lys Ile Lys Lys Leu Glu Glu Val Arg Lys Glu Leu Val
158 145             150             155             160
161 Asn Lys Ile Arg Asn Lys Lys Ala Leu Leu Gln Glu Ile Glu Lys Gln
162              165             170             175
165 Phe Asp Asp Leu Gln Asn Ile Lys Leu Arg Asn Gln Thr Leu Glu Ser
166              180             185             190
169 Ser Ala Glu Asn Val Asn Gly Ile Arg Leu Pro Phe Val Leu Val Lys
170              195             200             205
173 Thr Ser Arg Lys Ala Arg Val Glu Ile Glu Ile Ser Asp Asp Ser Lys
174              210             215             220
177 Phe Ala His Phe Glu Phe Asn Gly Ala Pro Phe Thr Leu His Asp Asp
178 225             230             235             240
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190 <211> LENGTH: 1974
191 <212> TYPE: DNA
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194 <220> FEATURE:
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197 <223> OTHER INFORMATION:
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203 tccggcgagc cccccccgat gccctcctgc cttctctgaa gccgaagacg cccatcgctc      120
205 ccgggagtcg ggggtcccgc agcgcgcgat cgcgagatcg ggctt atg tct ggg ggc      177
206                               Met Ser Gly Gly
207                               1
209 ggc agg ccg ccg gct gcg caa aaa atc ctg cag tct ctg cgc ccg ccc      225
210 Gly Arg Pro Pro Ala Ala Gln Lys Ile Leu Gln Ser Leu Arg Pro Pro
211 5              10              15              20
213 ccg gtg ttc tcc acg ccg tcg cgg cct ccc ttc gcc tca ccc gac gac      273
214 Pro Val Phe Ser Thr Pro Ser Arg Pro Pro Phe Ala Ser Pro Asp Asp
215              25              30              35
217 tac cac cgc ttt cat gcg ccg act acc cct tct gcc act ggc tcc ggc      321
218 Tyr His Arg Phe His Ala Pro Thr Thr Pro Ser Ala Thr Gly Ser Gly
219              40              45              50

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221	ggc	atc	ggc	tcc	ggt	ggt	gtt	ggc	ggc	gat	att	gat	gag	ggg	ctt	gtt	369
222	Gly	Ile	Gly	Ser	Gly	Gly	Val	Gly	Gly	Asp	Ile	Asp	Glu	Gly	Leu	Val	
223			55				60					65					
225	atc	cgg	acg	cag	cta	aaa	aga	aaa	gcc	aca	cgc	gaa	gaa	aat	aat	gcg	417
226	Ile	Arg	Thr	Gln	Leu	Lys	Arg	Lys	Ala	Thr	Arg	Glu	Glu	Asn	Asn	Ala	
227		70					75					80					
229	gct	gag	tcg	agt	gac	tgt	atg	att	gtc	acc	act	gga	gtt	act	ggc	aat	465
230	Ala	Glu	Ser	Ser	Asp	Cys	Met	Ile	Val	Thr	Thr	Gly	Val	Thr	Gly	Asn	
231	85					90						95				100	
233	ccg	cta	ctc	acc	cca	gtg	tct	gga	aaa	gct	gtt	aag	aat	tct	aaa	tca	513
234	Pro	Leu	Leu	Thr	Pro	Val	Ser	Gly	Lys	Ala	Val	Lys	Asn	Ser	Lys	Ser	
235				105						110					115		
237	aag	act	aag	aac	aat	aaa	gct	ggg	cct	cag	aca	cct	acg	cca	aat	gtt	561
238	Lys	Thr	Lys	Asn	Asn	Lys	Ala	Gly	Pro	Gln	Thr	Pro	Thr	Pro	Asn	Val	
239				120					125					130			
241	ggc	tca	cca	ctc	aat	cca	tca	act	cct	gct	ggt	act	tgc	cgc	tat	gac	609
242	Gly	Ser	Pro	Leu	Asn	Pro	Ser	Thr	Pro	Ala	Gly	Thr	Cys	Arg	Tyr	Asp	
243			135					140					145				
245	agt	tcg	tta	gga	ctt	ctg	aca	aag	aag	ttc	atc	aat	ttg	ctg	aag	caa	657
246	Ser	Ser	Leu	Gly	Leu	Leu	Thr	Lys	Lys	Phe	Ile	Asn	Leu	Leu	Lys	Gln	
247		150					155					160					
249	gct	gag	gat	ggc	att	cta	gat	ttg	aat	aat	gct	gca	gaa	aca	cta	gag	705
250	Ala	Glu	Asp	Gly	Ile	Leu	Asp	Leu	Asn	Asn	Ala	Ala	Glu	Thr	Leu	Glu	
251	165					170					175					180	
253	gtt	caa	aag	cga	cgc	ata	tat	gac	atc	aca	aat	gtc	ctc	gaa	gga	att	753
254	Val	Gln	Lys	Arg	Arg	Ile	Tyr	Asp	Ile	Thr	Asn	Val	Leu	Glu	Gly	Ile	
255				185						190					195		
257	ggt	ctt	ata	gaa	aag	aca	ctt	aaa	aac	aga	att	cgt	tgg	aag	ggc	ttg	801
258	Gly	Leu	Ile	Glu	Lys	Thr	Leu	Lys	Asn	Arg	Ile	Arg	Trp	Lys	Gly	Leu	
259			200						205					210			
261	gat	gat	tca	gga	gtg	gaa	tta	gat	aat	ggc	ctt	tca	ggt	ttg	cag	aca	849
262	Asp	Asp	Ser	Gly	Val	Glu	Leu	Asp	Asn	Gly	Leu	Ser	Gly	Leu	Gln	Thr	
263			215					220					225				
265	gaa	gtt	gaa	aat	ctt	aat	ttg	cag	gag	caa	gcc	tta	gat	gag	cgt	ata	897
266	Glu	Val	Glu	Asn	Leu	Asn	Leu	Gln	Glu	Gln	Ala	Leu	Asp	Glu	Arg	Ile	
267		230					235					240					
269	agt	gat	atg	cgc	gaa	aag	cta	agg	ggg	tta	acg	gaa	gat	gag	aac	agt	945
270	Ser	Asp	Met	Arg	Glu	Lys	Leu	Arg	Gly	Leu	Thr	Glu	Asp	Glu	Asn	Ser	
271	245					250						255				260	
273	caa	aga	tgg	ctc	tat	gtg	acg	gaa	gat	gat	atc	aag	gga	tta	ccc	tgc	993
274	Gln	Arg	Trp	Leu	Tyr	Val	Thr	Glu	Asp	Asp	Ile	Lys	Gly	Leu	Pro	Cys	
275				265						270					275		
277	ttt	cag	aat	gaa	act	cta	att	gca	ata	aaa	gct	cct	cat	ggt	act	aca	1041
278	Phe	Gln	Asn	Glu	Thr	Leu	Ile	Ala	Ile	Lys	Ala	Pro	His	Gly	Thr	Thr	
279				280					285					290			
281	ctt	gaa	gta	cct	gat	cct	gat	gag	gct	ggt	gat	tat	ctc	cag	agg	aga	1089
282	Leu	Glu	Val	Pro	Asp	Pro	Asp	Glu	Ala	Gly	Asp	Tyr	Leu	Gln	Arg	Arg	
283			295					300					305				
285	tac	aga	atc	gta	tta	aga	agt	acc	ctg	ggt	cca	ata	gat	gtt	tac	tta	1137

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289 gtt agt caa ttt gac gat gga ttt gag aat ttg ggt ggt gct gcg aca      1185
290 Val Ser Gln Phe Asp Asp Gly Phe Glu Asn Leu Gly Gly Ala Ala Thr
291 325                      330                      335                      340
293 cct cca agg cat aca aat gtc cca aaa cct gga cct tgt gaa gac tta      1233
294 Pro Pro Arg His Thr Asn Val Pro Lys Pro Gly Pro Cys Glu Asp Leu
295                      345                      350                      355
297 cat gca aca aac gct aca caa agc agc aaa tca atc aat gtg gaa tat      1281
298 His Ala Thr Asn Ala Thr Gln Ser Ser Lys Ser Ile Asn Val Glu Tyr
299                      360                      365                      370
301 aat att cag cac agg cag aat act cca caa gat cct agt tct tca aat      1329
302 Asn Ile Gln His Arg Gln Asn Thr Pro Gln Asp Pro Ser Ser Ser Asn
303                      375                      380                      385
305 gat tat gga ggg atg aca agg ata atc cct tca gat gtt aat act gat      1377
306 Asp Tyr Gly Gly Met Thr Arg Ile Ile Pro Ser Asp Val Asn Thr Asp
307                      390                      395                      400
309 gct gat tac tgg ctc cta aca gag ggt gat gtt agt att act gac atg      1425
310 Ala Asp Tyr Trp Leu Leu Thr Glu Gly Asp Val Ser Ile Thr Asp Met
311 405                      410                      415                      420
313 tgg gaa aca gca cca gaa gtg cag tgg gac acc gct gtg ttt tta cct      1473
314 Trp Glu Thr Ala Pro Glu Val Gln Trp Asp Thr Ala Val Phe Leu Pro
315                      425                      430                      435
317 gaa gat gtt agc atc cca cat gca cat cat agt ccg cgg atg cag gtt      1521
318 Glu Asp Val Ser Ile Pro His Ala His His Ser Pro Arg Met Gln Val
319                      440                      445                      450
321 cca agc atg gat caa cca taagggtcatg gcgggtgaaaaa cttgacatat      1569
322 Pro Ser Met Asp Gln Pro
323                      455
325 ggaatttcctg gagtgcgtgtt tcagaaaata ctgatttcaa aatggaaaga tcagggcagc      1629
327 aagttcagac tgatcaccgt tctgaatttg ctgtttgtta tggagacgat tgggtgccaac      1689
329 taacttatca gtctgctgcc ttgtttgttc tggcacctgt ccttcagttg aaaaggcgcc      1749
331 catgtgcata ttgcaccttg aattcgggct gctatgcaca ttcgggtatct gctttatttc      1809
333 tctaactgag tatattttgc aaggcaatag tggtctgtga gctctcttgg gaattaatac      1869
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352      20      25      30
355 Ser Pro Asp Asp Tyr His Arg Phe His Ala Pro Thr Thr Pro Ser Ala
356      35      40      45
359 Thr Gly Ser Gly Gly Ile Gly Ser Gly Gly Val Gly Gly Asp Ile Asp
360      50      55      60

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VERIFICATION SUMMARY

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L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date